



# SEQUENCE LISTING

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STROMINGER, Jack L

<120> MONOVALENT, MULTIVALENT AND MULTIMERIC MHC BINDING  
DOMAIN FUSION PROTEINS AND CONJUGATES, AND USES  
THEREFOR

<130> HUIP-P01-005

<140> 09/248,964

<141> 1999-02-12

<150> PCT/US97/14503

<151> 1997-08-15

<150> 60/075,351

<151> 1998-02-19

<150> 60/024,077

<151> 1996-08-15

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 750

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-Fos fusion

<220>

<221> CDS

<222> (1)..(735)

<220>

<221> misc\_feature

<222> (1)..(21)

<223> 3' end of secretory signal

<220>

<221> misc\_structure

<222> (22)..(594)

<223> DRA\*0101 extracellular domain

<220>

<221> misc\_feature

<222> (595)..(615)

<223> Linker sequence

<220>

<221> misc\_feature

<222> (616)..(735)

<223> Fos leucine zipper domain

<400> 1

gta tct ctc gag aaa aga gag atc aaa gaa gaa cat gtg atc atc cag	48
Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln	
1 5 10 15	
gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac	96
Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp	
20 25 30	
ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg	144
Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr	
35 40 45	
gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa	192
Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln	
50 55 60	
ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg	240
Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met	
65 70 75 80	
aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta	288
Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val	
85 90 95	
act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc	336
Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu	
100 105 110	
atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg	384
Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp	
115 120 125	
ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc	432
Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe	
130 135 140	
ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc	480
Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe	
145 150 155 160	
ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc	528
Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly	
165 170 175	
ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct	576
Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro	
180 185 190	
ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat	624
Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp	
195 200 205	
aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg	672
Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu	
210 215 220	

cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc 720  
 Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe  
 225 230 235 240

atc ctg gcc gcc cat tgagaattct atgac 750  
 Ile Leu Ala Ala His  
 245

<210> 2  
 <211> 245  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: DR2-Fos fusion

<220>  
 <221> misc\_feature  
 <222> (1)..(7)  
 <223> 3' end of secretory signal

<220>  
 <221> misc\_structure  
 <222> (8)..(198)  
 <223> DRA\*0101 extracellular domain

<220>  
 <221> misc\_feature  
 <222> (199)..(205)  
 <223> Linker sequence

<220>  
 <221> misc\_feature  
 <222> (206)..(245)  
 <223> Fos leucine zipper domain

<400> 2  
 Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln  
 1 5 10 15  
 Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp  
 20 25 30  
 Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr  
 35 40 45  
 Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln  
 50 55 60  
 Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met  
 65 70 75 80  
 Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val  
 85 90 95  
 Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu  
 100 105 110

Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp  
 115 120 125  
 Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe  
 130 135 140  
 Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe  
 145 150 155 160  
 Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly  
 165 170 175  
 Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro  
 180 185 190  
 Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp  
 195 200 205  
 Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu  
 210 215 220  
 Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe  
 225 230 235 240  
 Ile Leu Ala Ala His  
 245

<210> 3

<211> 771

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-Jun fusion

<220>

<221> CDS

<222> (1)..(756)

<220>

<221> misc\_feature

<222> (1)..(21)

<223> 3' end of secretory signal

<220>

<221> misc\_feature

<222> (22)..(615)

<223> DRB1\*1501 extracellular domain

<220>

<221> misc\_feature

<222> (616)..(636)

<223> Linker sequence

<220>

<221> misc\_feature

<222> (637)..(756)

<223> Jun leucine zipper domain

<400> 3

gta tct ctc gag aaa aga gag ggg gac acc cga cca cgt ttc ctg tgg	48
Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp	
1 5 10 15	
cag cct aag agg gag tgt cat ttc ttc aat ggg acg gag cgg gtg cgg	96
Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg	
20 25 30	
ttc ctg gac aga tac ttc tat aac cag gag gag tcc gtg cgc ttc gac	144
Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp	
35 40 45	
agc gac gtg ggg gag ttc cgg gcg gtg acg gag ctg ggg cgg cct gac	192
Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp	
50 55 60	
gct gag tac tgg aac agc cag aag gac atc ctg gag cag gcg cgg gcc	240
Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala	
65 70 75 80	
gcg gtg gac acc tac tgc aga cac aac tac ggg gtt gtg gag agc ttc	288
Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe	
85 90 95	
aca gtg cag cgg cga gtc caa cct aag gtg act gta tat cct tca aag	336
Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys	
100 105 110	
acc cag ccc ctg cag cac cac aac ctc ctg gtc tgc tct gtg agt ggt	384
Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly	
115 120 125	
ttc tat cca ggc agc att gaa gtc agg tgg ttc ctg aac ggc cag gaa	432
Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu	
130 135 140	
gag aag gct ggg atg gtg tcc aca ggc ctg atc cag aat gga gac tgg	480
Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp	
145 150 155 160	
acc ttc cag acc ctg gtg atg ctg gaa aca gtt cct cga agt gga gag	528
Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu	
165 170 175	
gtt tac acc tgc caa gtg gag cac cca agc gtg aca agc cct ctc aca	576
Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr	
180 185 190	
gtg gaa tgg aga gca cgg tct gaa tct gca cag agc aag gtc gac gga	624
Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly	
195 200 205	

ggt ggc ggc ggt cgc atc gcc cgg ctc gag gaa aaa gtg aaa acc ttg 672  
 Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu  
 210 215 220

aaa gct cag aac tcg gag ctc gcg tcc acg gcc aac atg ctc agg gaa 720  
 Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu  
 225 230 235 240

cag gtg gca cag ctt aaa cag aaa gtc atg aac cat tgagaattct atgac 771  
 Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His  
 245 250

<210> 4  
 <211> 252  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: DR2-Jun fusion

<220>  
 <221> misc\_feature  
 <222> (1)..(7)  
 <223> 3' end of secretory signal

<220>  
 <221> misc\_feature  
 <222> (8)..(205)  
 <223> DRB1\*1501 extracellular domain

<220>  
 <221> misc\_feature  
 <222> (206)..(212)  
 <223> Linker sequence

<220>  
 <221> misc\_feature  
 <222> (213)..(252)  
 <223> Jun leucine zipper domain

<400> 4  
 Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp  
 1 5 10 15

Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg  
 20 25 30

Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp  
 35 40 45

Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp  
 50 55 60

Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala  
 65 70 75 80

Ala	Val	Asp	Thr	Tyr	Cys	Arg	His	Asn	Tyr	Gly	Val	Val	Glu	Ser	Phe	
				85					90					95		
Thr	Val	Gln	Arg	Arg	Val	Gln	Pro	Lys	Val	Thr	Val	Tyr	Pro	Ser	Lys	
		100						105					110			
Thr	Gln	Pro	Leu	Gln	His	His	Asn	Leu	Leu	Val	Cys	Ser	Val	Ser	Gly	
		115					120					125				
Phe	Tyr	Pro	Gly	Ser	Ile	Glu	Val	Arg	Trp	Phe	Leu	Asn	Gly	Gln	Glu	
	130					135					140					
Glu	Lys	Ala	Gly	Met	Val	Ser	Thr	Gly	Leu	Ile	Gln	Asn	Gly	Asp	Trp	
145					150					155					160	
Thr	Phe	Gln	Thr	Leu	Val	Met	Leu	Glu	Thr	Val	Pro	Arg	Ser	Gly	Glu	
			165						170					175		
Val	Tyr	Thr	Cys	Gln	Val	Glu	His	Pro	Ser	Val	Thr	Ser	Pro	Leu	Thr	
		180						185					190			
Val	Glu	Trp	Arg	Ala	Arg	Ser	Glu	Ser	Ala	Gln	Ser	Lys	Val	Asp	Gly	
	195						200					205				
Gly	Gly	Gly	Gly	Arg	Ile	Ala	Arg	Leu	Glu	Glu	Lys	Val	Lys	Thr	Leu	
	210					215					220					
Lys	Ala	Gln	Asn	Ser	Glu	Leu	Ala	Ser	Thr	Ala	Asn	Met	Leu	Arg	Glu	
225					230					235					240	
Gln	Val	Ala	Gln	Leu	Lys	Gln	Lys	Val	Met	Asn	His					
			245						250							

<210> 5  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic PCR primer

<400> 5  
 gtatctctcg agaaaagaga gatcaaagaa gaacatgtga tc 42

<210> 6  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic PCR primer

<400> 6  
 gtcataagaat tctcaatggg cggccaggat gaactccag 39

<210> 7  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 7  
gtatctctcg agaaaagaga gggggacacc cgaccacgtt tc 42

<210> 8  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 8  
gtcatagaat tctcaatggt tcatgacttt ctgtttaag 39

<210> 9  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic,  
biotin ligase recognition sequence

<400> 9  
Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp  
1 5 10

<210> 10  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic,  
linker sequence

<400> 10  
Ser Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

<210> 11  
<211> 1446



<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: DR2-IgG fusion

<220>  
<221> CDS  
<222> (1)..(1437)

<220>  
<221> misc\_feature  
<222> (1)..(15)  
<223> 3' end of secretory signal

<220>  
<221> misc\_feature  
<222> (16)..(588)  
<223> DRA\*0101 extracellular domain

<220>  
<221> misc\_feature  
<222> (589)..(609)  
<223> Linker

<220>  
<221> misc\_feature  
<222> (610)..(729)  
<223> Fos leucine zipper domain

<220>  
<221> misc\_feature  
<222> (730)..(1437)  
<223> IgG domain

<400> 11  
ctc gag aaa aga gag atc aaa gaa gaa cat gtg atc atc cag gcc gag 48  
Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu  
1 5 10 15  
  
ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac ttt gat 96  
Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp  
20 25 30  
  
ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg gtc tgg 144  
Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp  
35 40 45  
  
cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa ggt gca 192  
Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala  
50 55 60  
  
ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg aca aag 240  
Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys  
65 70 75 80

cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta act gtg	288
Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val	
85 90 95	
ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc atc tgt	336
Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys	
100 105 110	
ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg ctt cga	384
Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg	
115 120 125	
aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc ctg ccc	432
Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro	
130 135 140	
agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc ctg ccc	480
Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro	
145 150 155 160	
tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc ttg gat	528
Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp	
165 170 175	
gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct ctc cca	576
Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro	
180 185 190	
gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat aca ctc	624
Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp Thr Leu	
195 200 205	
caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg cag acc	672
Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr	
210 215 220	
gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc atc ctg	720
Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu	
225 230 235 240	
gcc gcc cat gca gca tct gag ccc aga ggg ccc aca atc aag ccc tgt	768
Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys	
245 250 255	
cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc	816
Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val	
260 265 270	
ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc ctg agc	864
Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser	
275 280 285	
ccc ata gtc aca tgt gtg gtg gtg gat gtg agc gag gat gac cca gat	912
Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp	
290 295 300	

gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag	960
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln	
305 310 315 320	
aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt	1008
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser	
325 330 335	
gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa	1056
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys	
340 345 350	
tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc	1104
Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile	
355 360 365	
tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct	1152
Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro	
370 375 380	
cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg	1200
Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met	
385 390 395 400	
gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac	1248
Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn	
405 410 415	
ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct	1296
Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser	
420 425 430	
gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac	1344
Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn	
435 440 445	
tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg	1392
Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu	
450 455 460	
cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt aaa	1437
His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys	
465 470 475	
tgagaattc	1446

<210> 12

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-IgG fusion

<220>

<221> misc\_feature

<222> (1)..(5)  
<223> 3' end of secretory signal

<220>  
<221> misc\_feature  
<222> (6)..(196)  
<223> DRA\*0101 extracellular domain

<220>  
<221> misc\_feature  
<222> (197)..(203)  
<223> Linker

<220>  
<221> misc\_feature  
<222> (204)..(243)  
<223> Fos leucine zipper domain

<220>  
<221> misc\_feature  
<222> (244)..(479)  
<223> IgG domain

<400> 12  
Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu  
1 5 10 15

Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp  
20 25 30

Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp  
35 40 45

Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala  
50 55 60

Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys  
65 70 75 80

Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val  
85 90 95

Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys  
100 105 110

Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg  
115 120 125

Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro  
130 135 140

Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro  
145 150 155 160

Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp

165					170					175					
Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro	Ser	Pro	Leu	Pro
		180						185					190		
Glu	Thr	Thr	Glu	Val	Asp	Gly	Gly	Gly	Gly	Gly	Leu	Thr	Asp	Thr	Leu
		195					200					205			
Gln	Ala	Glu	Thr	Asp	Gln	Leu	Glu	Asp	Glu	Lys	Ser	Ala	Leu	Gln	Thr
	210					215					220				
Glu	Ile	Ala	Asn	Leu	Leu	Lys	Glu	Lys	Glu	Lys	Leu	Glu	Phe	Ile	Leu
225				230					235						240
Ala	Ala	His	Ala	Ala	Ser	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys
			245						250					255	
Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val
		260						265					270		
Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser
	275						280					285			
Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp
	290					295					300				
Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln
305					310					315					320
Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser
			325						330				335		
Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys
		340						345					350		
Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile
	355						360					365			
Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro
	370					375					380				
Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met
385					390					395					400
Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn
			405						410					415	
Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser
		420						425					430		
Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn
	435						440					445			
Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu
	450					455					460				
His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys	

465

470

475

&lt;210&gt; 13

&lt;211&gt; 1851

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: DR2-IgM fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1836)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(75)

&lt;223&gt; 3' end of secretory signal

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (76)..(648)

&lt;223&gt; DRA\*0101 extracellular domain

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (649)..(669)

&lt;223&gt; Linker

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (670)..(789)

&lt;223&gt; Fos leucine zipper domain

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (790)..(1836)

&lt;223&gt; IgG domain

&lt;400&gt; 13

atg gcc ata agt gga gtc cct gtg cta gga ttt ttc atc ata gct gtg 48

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val

1

5

10

15

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc 96

Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile

20

25

30

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg 144

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met

35

40

45

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag 192

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys

50

55

60

gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag	240
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu	
65 70 75 80	
gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa	288
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu	
85 90 95	
atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca	336
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro	
100 105 110	
gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac	384
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn	
115 120 125	
gtc ctc atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc	432
Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val	
130 135 140	
acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca	480
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr	
145 150 155 160	
gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc	528
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu	
165 170 175	
ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac	576
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His	
180 185 190	
tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca	624
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro	
195 200 205	
agc cct ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta	672
Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu	
210 215 220	
act gat aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct	720
Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser	
225 230 235 240	
gcg ttg cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg	768
Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu	
245 250 255	
gag ttc atc ctg gcc gcc cac gtc gca gaa atg aac ccc aat gta aat	816
Glu Phe Ile Leu Ala Ala His Val Ala Glu Met Asn Pro Asn Val Asn	
260 265 270	
gtg ttc gtc cca cca cgg gat ggc ttc tct ggc cct gca cca cgc aag	864
Val Phe Val Pro Pro Arg Asp Gly Phe Ser Gly Pro Ala Pro Arg Lys	
275 280 285	
tct aaa ctc atc tgc gag gcc acg aac ttc act cca aaa ccg atc aca	912

Ser	Lys	Leu	Ile	Cys	Glu	Ala	Thr	Asn	Phe	Thr	Pro	Lys	Pro	Ile	Thr		
290						295					300						
gta	tcc	tgg	cta	aag	gat	ggg	aag	ctc	gtg	gaa	tct	ggc	ttc	acc	aca	960	
Val	Ser	Trp	Leu	Lys	Asp	Gly	Lys	Leu	Val	Glu	Ser	Gly	Phe	Thr	Thr		
305					310					315					320		
gat	ccg	gtg	acc	atc	gag	aac	aaa	gga	tcc	aca	ccc	caa	acc	tac	aag	1008	
Asp	Pro	Val	Thr	Ile	Glu	Asn	Lys	Gly	Ser	Thr	Pro	Gln	Thr	Tyr	Lys		
				325					330					335			
gtc	ata	agc	aca	ctt	acc	atc	tct	gaa	atc	gac	tgg	ctg	aac	ctg	aat	1056	
Val	Ile	Ser	Thr	Leu	Thr	Ile	Ser	Glu	Ile	Asp	Trp	Leu	Asn	Leu	Asn		
			340					345					350				
gtg	tac	acc	tgc	cgt	gtg	gat	cac	agg	ggc	ctc	acc	ttc	ttg	aag	aac	1104	
Val	Tyr	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Leu	Lys	Asn		
		355					360					365					
gtg	tcc	tcc	aca	tgt	gct	gcc	agt	ccc	tcc	aca	gat	atc	ctt	aat	ttt	1152	
Val	Ser	Ser	Thr	Cys	Ala	Ala	Ser	Pro	Ser	Thr	Asp	Ile	Leu	Asn	Phe		
	370					375					380						
act	att	cct	cct	tcc	ttt	gcc	gac	atc	ttc	ctt	agc	aag	tcc	gct	aac	1200	
Thr	Ile	Pro	Pro	Ser	Phe	Ala	Asp	Ile	Phe	Leu	Ser	Lys	Ser	Ala	Asn		
385					390					395					400		
ctg	acc	tgt	ctg	gtc	tca	aac	ctg	gca	acc	tat	gaa	acc	ctg	agt	atc	1248	
Leu	Thr	Cys	Leu	Val	Ser	Asn	Leu	Ala	Thr	Tyr	Glu	Thr	Leu	Ser	Ile		
				405					410					415			
tcc	tgg	gct	tct	caa	agt	ggc	gaa	cca	ctg	gaa	acc	aaa	att	aaa	atc	1296	
Ser	Trp	Ala	Ser	Gln	Ser	Gly	Glu	Pro	Leu	Glu	Thr	Lys	Ile	Lys	Ile		
			420				425						430				
atg	gaa	agc	cat	ccc	aat	ggc	acc	ttc	agt	gct	aag	ggc	gtg	gct	agt	1344	
Met	Glu	Ser	His	Pro	Asn	Gly	Thr	Phe	Ser	Ala	Lys	Gly	Val	Ala	Ser		
		435				440					445						
gtt	tgt	gtg	gaa	gac	tgg	aat	aac	agg	aag	gaa	ttt	gtg	tgt	act	gtg	1392	
Val	Cys	Val	Glu	Asp	Trp	Asn	Asn	Arg	Lys	Glu	Phe	Val	Cys	Thr	Val		
	450					455					460						
act	cac	agg	gat	ctg	cct	tca	cca	cag	aag	aaa	ttc	atc	tca	aaa	ccc	1440	
Thr	His	Arg	Asp	Leu	Pro	Ser	Pro	Gln	Lys	Lys	Phe	Ile	Ser	Lys	Pro		
465					470					475					480		
aat	gag	gtg	cac	aaa	cat	cca	cct	gct	gtg	tac	ctg	ctg	cca	cca	gct	1488	
Asn	Glu	Val	His	Lys	His	Pro	Pro	Ala	Val	Tyr	Leu	Leu	Pro	Pro	Ala		
				485					490					495			
cgt	gaa	caa	ctg	aac	ctg	agg	gag	tca	gcc	aca	gtc	acc	tgc	ctg	gtg	1536	
Arg	Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Val	Thr	Cys	Leu	Val		
			500					505					510				
aag	ggc	ttc	tct	cct	gca	gac	atc	tct	gtg	caa	tgg	aag	cag	agg	ggc	1584	
Lys	Gly	Phe	Ser	Pro	Ala	Asp	Ile	Ser	Val	Gln	Trp	Lys	Gln	Arg	Gly		



515	520	525	
cag ctc tta ccc cag gag aag tat gtg acc agt gcc ccg atg cca gag			1632
Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu			
530	535	540	
cct ggg gcc cca ggc ttc tac ttt acc cac agc atc ctg act gtg aca			1680
Pro Gly Ala Pro Gly Phe Tyr Phe Thr His Ser Ile Leu Thr Val Thr			
545	550	555	560
gag gag gaa tgg aac tcc gga gag acc tat acc tgt gtt gta ggc cac			1728
Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His			
565	570	575	
gag gcc ctg cca cac ctg gtg acc gag agg acc gtg gac aag tcc act			1776
Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr			
580	585	590	
ggt aaa ccc aca ctg tac aat gtc tcc ctg atc atg tct gac aca ggc			1824
Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly			
595	600	605	
ggc acc tgc tat tgaagatctg tcgac			1851
Gly Thr Cys Tyr			
610			

<210> 14  
 <211> 612  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: DR2-IgM fusion

<220>  
 <221> misc\_feature  
 <222> (1)..(25)  
 <223> 3' end of secretory signal

<220>  
 <221> misc\_feature  
 <222> (26)..(216)  
 <223> DRA\*0101 extracellular domain

<220>  
 <221> misc\_feature  
 <222> (217)..(223)  
 <223> Linker

<220>  
 <221> misc\_feature  
 <222> (224)..(263)  
 <223> Fos leucine zipper domain

<220>  
 <221> misc\_feature  
 <222> (264)..(612)

<223> IgG domain

<400> 14

Met	Ala	Ile	Ser	Gly	Val	Pro	Val	Leu	Gly	Phe	Phe	Ile	Ile	Ala	Val
1				5					10					15	
Leu	Met	Ser	Ala	Gln	Glu	Ser	Trp	Ala	Ile	Lys	Glu	Glu	His	Val	Ile
			20					25					30		
Ile	Gln	Ala	Glu	Phe	Tyr	Leu	Asn	Pro	Asp	Gln	Ser	Gly	Glu	Phe	Met
		35					40					45			
Phe	Asp	Phe	Asp	Gly	Asp	Glu	Ile	Phe	His	Val	Asp	Met	Ala	Lys	Lys
	50					55					60				
Glu	Thr	Val	Trp	Arg	Leu	Glu	Glu	Phe	Gly	Arg	Phe	Ala	Ser	Phe	Glu
65					70					75					80
Ala	Gln	Gly	Ala	Leu	Ala	Asn	Ile	Ala	Val	Asp	Lys	Ala	Asn	Leu	Glu
				85					90					95	
Ile	Met	Thr	Lys	Arg	Ser	Asn	Tyr	Thr	Pro	Ile	Thr	Asn	Val	Pro	Pro
			100					105					110		
Glu	Val	Thr	Val	Leu	Thr	Asn	Ser	Pro	Val	Glu	Leu	Arg	Glu	Pro	Asn
			115				120					125			
Val	Leu	Ile	Cys	Phe	Ile	Asp	Lys	Phe	Thr	Pro	Pro	Val	Val	Asn	Val
	130					135					140				
Thr	Trp	Leu	Arg	Asn	Gly	Lys	Pro	Val	Thr	Thr	Gly	Val	Ser	Glu	Thr
145					150					155					160
Val	Phe	Leu	Pro	Arg	Glu	Asp	His	Leu	Phe	Arg	Lys	Phe	His	Tyr	Leu
				165					170					175	
Pro	Phe	Leu	Pro	Ser	Thr	Glu	Asp	Val	Tyr	Asp	Cys	Arg	Val	Glu	His
			180					185					190		
Trp	Gly	Leu	Asp	Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro
		195					200					205			
Ser	Pro	Leu	Pro	Glu	Thr	Thr	Glu	Val	Asp	Gly	Gly	Gly	Gly	Gly	Leu
	210					215					220				
Thr	Asp	Thr	Leu	Gln	Ala	Glu	Thr	Asp	Gln	Leu	Glu	Asp	Glu	Lys	Ser
225				230					235					240	
Ala	Leu	Gln	Thr	Glu	Ile	Ala	Asn	Leu	Leu	Lys	Glu	Lys	Glu	Lys	Leu
				245					250					255	
Glu	Phe	Ile	Leu	Ala	Ala	His	Val	Ala	Glu	Met	Asn	Pro	Asn	Val	Asn
			260					265					270		
Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Ser	Gly	Pro	Ala	Pro	Arg	Lys
		275					280					285			

Ser	Lys	Leu	Ile	Cys	Glu	Ala	Thr	Asn	Phe	Thr	Pro	Lys	Pro	Ile	Thr	290	295	300	
Val	Ser	Trp	Leu	Lys	Asp	Gly	Lys	Leu	Val	Glu	Ser	Gly	Phe	Thr	Thr	305	310	315	320
Asp	Pro	Val	Thr	Ile	Glu	Asn	Lys	Gly	Ser	Thr	Pro	Gln	Thr	Tyr	Lys	325	330	335	
Val	Ile	Ser	Thr	Leu	Thr	Ile	Ser	Glu	Ile	Asp	Trp	Leu	Asn	Leu	Asn	340	345	350	
Val	Tyr	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Leu	Lys	Asn	355	360	365	
Val	Ser	Ser	Thr	Cys	Ala	Ala	Ser	Pro	Ser	Thr	Asp	Ile	Leu	Asn	Phe	370	375	380	
Thr	Ile	Pro	Pro	Ser	Phe	Ala	Asp	Ile	Phe	Leu	Ser	Lys	Ser	Ala	Asn	385	390	395	400
Leu	Thr	Cys	Leu	Val	Ser	Asn	Leu	Ala	Thr	Tyr	Glu	Thr	Leu	Ser	Ile	405	410	415	
Ser	Trp	Ala	Ser	Gln	Ser	Gly	Glu	Pro	Leu	Glu	Thr	Lys	Ile	Lys	Ile	420	425	430	
Met	Glu	Ser	His	Pro	Asn	Gly	Thr	Phe	Ser	Ala	Lys	Gly	Val	Ala	Ser	435	440	445	
Val	Cys	Val	Glu	Asp	Trp	Asn	Asn	Arg	Lys	Glu	Phe	Val	Cys	Thr	Val	450	455	460	
Thr	His	Arg	Asp	Leu	Pro	Ser	Pro	Gln	Lys	Lys	Phe	Ile	Ser	Lys	Pro	465	470	475	480
Asn	Glu	Val	His	Lys	His	Pro	Pro	Ala	Val	Tyr	Leu	Leu	Pro	Pro	Ala	485	490	495	
Arg	Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Val	Thr	Cys	Leu	Val	500	505	510	
Lys	Gly	Phe	Ser	Pro	Ala	Asp	Ile	Ser	Val	Gln	Trp	Lys	Gln	Arg	Gly	515	520	525	
Gln	Leu	Leu	Pro	Gln	Glu	Lys	Tyr	Val	Thr	Ser	Ala	Pro	Met	Pro	Glu	530	535	540	
Pro	Gly	Ala	Pro	Gly	Phe	Tyr	Phe	Thr	His	Ser	Ile	Leu	Thr	Val	Thr	545	550	555	560
Glu	Glu	Glu	Trp	Asn	Ser	Gly	Glu	Thr	Tyr	Thr	Cys	Val	Val	Gly	His	565	570	575	
Glu	Ala	Leu	Pro	His	Leu	Val	Thr	Glu	Arg	Thr	Val	Asp	Lys	Ser	Thr	580	585	590	

Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly  
595 600 605

Gly Thr Cys Tyr  
610